DNA methylation fingerprint of neuroblastoma reveals new biological and clinical insights.

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Public Summary:
We performed epigenetic analysis of neuroblastoma, which provides new insights into the pathogenesis and clinical behavior of this pediatric tumor.

Scientific Abstract:
AIM: To define the DNA methylation landscape of neuroblastoma and its clinicopathological impact. MATERIALS & METHODS: Microarray DNA methylation data were analyzed and associated with functional/regulatory genome annotation data, transcriptional profiles and clinicobiological parameters. RESULTS: DNA methylation changes in neuroblastoma affect not only promoters but also intragenic and intergenic regions at cytosine-phosphate-guanine (CpG) and non-CpG sites, and target functional chromatin domains of development and cancer-related genes such as CCND1. Tumors with diverse clinical risk showed differences affecting CpG and, remarkably, non-CpG sites. Non-CpG methylation observed essentially in clinically favorable cases was associated with the differentiation status of neuroblastoma and expression of key genes such as ALK. CONCLUSION: This epigenetic fingerprint of neuroblastoma provides new insights into the pathogenesis and clinical behavior of this pediatric tumor.